

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/314,889DATE: 06/24/1999
TIME: 11:52:57

INPUT SET: S32352.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Yu, Guo-Liang
6 Ni, Jian
7 Dixit, Vishva
8 Gentz, Reiner L.
9 Dillon, Patrick J.
10
11 (ii) TITLE OF INVENTION: Death Domain Containing Receptors
12
13 (iii) NUMBER OF SEQUENCES: 17
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
17 (B) STREET: 1100 New York Ave., NW, Suite 600
18 (C) CITY: Washington
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005-3934
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 09/314,889
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/815,469
36 (B) FILING DATE:
37
38 (vii) PRIOR APPLICATION DATA:
39 (A) APPLICATION NUMBER: US 60/028,711
40 (B) FILING DATE: 17-OCT-1996
41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: US 60/013,285
44 (B) FILING DATE: 12-MAR-1996
45
46 (viii) ATTORNEY/AGENT INFORMATION:

ENTERED

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INPUT SET: S32352.raw

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47      (A) NAME: Steffe, Eric K.
48      (B) REGISTRATION NUMBER: 36,688
49      (C) REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
50
51      (ix) TELECOMMUNICATION INFORMATION:
52          (A) TELEPHONE: 202-371-2600
53          (B) TELEFAX: 202-371-2540
54
55
56      (2) INFORMATION FOR SEQ ID NO:1:
57
58          (i) SEQUENCE CHARACTERISTICS:
59              (A) LENGTH: 1783 base pairs
60              (B) TYPE: nucleic acid
61              (C) STRANDEDNESS: double
62              (D) TOPOLOGY: both
63
64          (ii) MOLECULE TYPE: cDNA
65
66
67          (ix) FEATURE:
68              (A) NAME/KEY: CDS
69              (B) LOCATION: 198..1481
70
71
72          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
73
74      CATGGGTGGG GGTGGGGGCG CTGCTGGATT CCTGCTCTGG TGGAGGGGAA ACTTGTGAGG      60
75
76      GGCTGGTAAG CGCCCCCTCC GAAGCCTGGT GTGTGCGCGG GGGGAAGGAA GTTAGTTTCC      120
77
78      TCTCCACCCA TGGGCACCCC TTCTGCCCCG GGCCTGGGAA GTGGGCTGCT CTGTGGGCAA      180
79
80      ATGCTGGGGC CTCTGAA ATG GAG GAG ACG CAG CAG GGA GAG GCC CCA CGT      230
81                      Met Glu Glu Thr Gln Gln Gly Glu Ala Pro Arg
82                      1              5              10
83
84      GGG CAG CTG CGC GGA GAG TCA GCA GCA CCT GTC CCC CAG GCG CTC CTC      278
85      Gly Gln Leu Arg Gly Glu Ser Ala Ala Pro Val Pro Gln Ala Leu Leu
86                      15              20              25
87
88      CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT CGT AGC CCC AGG      326
89      Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
90                      30              35              40
91
92      TGT GAC TGT GCC GGT GAC TTC CAC AAG AAG ATT GGT CTG TTT TGT TGC      374
93      Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
94                      45              50              55
95
96      AGA GGC TGC CCA GCG GGG CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC      422
97      Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
98                      60              65              70              75
99

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100	TGC	GGC	AAC	TCC	ACC	TGC	CTT	GTG	TGT	CCC	CAA	GAC	ACC	TTC	TTG	GCC	470
101	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
102					80					85					90		
103																	
104	TGG	GAG	AAC	CAC	CAT	AAT	TCT	GAA	TGT	GCC	CGC	TGC	CAG	GCC	TGT	GAT	518
105	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp	
106				95					100					105			
107																	
108	GAG	CAG	GCC	TCC	CAG	GTG	GCG	CTG	GAG	AAC	TGT	TCA	GCA	GTG	GCC	GAC	566
109	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	
110			110					115						120			
111																	
112	ACC	CGC	TGT	GGC	TGT	AAG	CCA	GGC	TGG	TTT	GTG	GAG	TGC	CAG	GTC	AGC	614
113	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	
114		125					130					135					
115																	
116	CAA	TGT	GTC	AGC	AGT	TCA	CCC	TTC	TAC	TGC	CAA	CCA	TGC	CTA	GAC	TGC	662
117	Gln	Cys	Val	Ser	Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	
118	140					145					150					155	
119																	
120	GGG	GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	GAT	ACT	710
121	Gly	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Cys	Ser	Arg	Arg	Arg	Asp	Thr	
122				160						165					170		
123																	
124	GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	CAT	GGC	GAT	GGC	TGC	758
125	Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	
126				175					180					185			
127																	
128	GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	806
129	Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	
130			190					195					200				
131																	
132	GCT	GTC	TGT	GGC	TGG	AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	854
133	Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	
134		205					210					215					
135																	
136	GGC	CTT	GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	TAC	902
137	Gly	Leu	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	
138	220					225					230					235	
139																	
140	CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	GAT	GAA	GCT	GGG	950
141	Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	
142				240						245					250		
143																	
144	ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	ACC	CAT	CTG	TCA	CCC	TTG	GAC	998
145	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	
146				255					260					265			
147																	
148	AGC	GCC	CAC	ACC	CTT	CTA	GCA	CCT	CCT	GAC	AGC	AGT	GAG	AAG	ATC	TGC	1046
149	Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	
150			270					275					280				
151																	
152	ACC	GTC	CAG	TTG	GTG	GGT	AAC	AGC	TGG	ACC	CCT	GGC	TAC	CCC	GAG	ACC	1094

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153 Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
154      285                      290                      295
155
156 CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC CAG TTG CCC      1142
157 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
158 300                      305                      310                      315
159
160 AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC ACA CTC TCG CCA GAG TCC      1190
161 Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
162                      320                      325                      330
163
164 CCA GCC GGC TCG CCA GCC ATG ATG CTG CAG CCG GGC CCG CAG CTC TAC      1238
165 Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
166                      335                      340                      345
167
168 GAC GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC      1286
169 Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
170                      350                      355                      360
171
172 ACG CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC      1334
173 Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile
174                      365                      370                      375
175
176 GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG      1382
177 Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln
178 380                      385                      390                      395
179
180 CAG CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG      1430
181 Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
182                      400                      405                      410
183
184 GGG CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC      1478
185 Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
186                      415                      420                      425
187
188 CCG TGACACGGCG CCCACTTGCC ACCTAGGCGC TCTGGTGGCC CTTGCAGAAG      1531
189 Pro
190
191
192 CCCTAAGTAC GGTTACTTAT GCGTGTAGAC ATTTTATGTC ACTTATTAAG CCGCTGGCAC      1591
193
194 GGCCCTGCGT AGCAGCACCA GCCGGCCCCA CCCCTGCTCG CCCCTATCGC TCCAGCCAAG      1651
195
196 GCGAAGAAGC ACGAACGAAT GTCGAGAGGG GGTGAAGACA TTTCTCAACT TCTCGGCCGG      1711
197
198 AGTTTGGCTG AGATCGCGGT ATTAAATCTG TGAAAGAAAA CAAAACAAAA CAAAAAAAAA      1771
199
200 AAAAAAAAAA AA      1783
201
202
203 (2) INFORMATION FOR SEQ ID NO:2:
204
205 (i) SEQUENCE CHARACTERISTICS:

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206 (A) LENGTH: 428 amino acids
207 (B) TYPE: amino acid
208 (D) TOPOLOGY: linear
209
210 (ii) MOLECULE TYPE: protein
211
212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
213
214 Met Glu Glu Thr Gln Gln Gly Glu Ala Pro Arg Gly Gln Leu Arg Gly
215 1 5 10 15
216
217 Glu Ser Ala Ala Pro Val Pro Gln Ala Leu Leu Leu Val Leu Leu Gly
218 20 25 30
219
220 Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg Cys Asp Cys Ala Gly
221 35 40 45
222
223 Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala
224 50 55 60
225
226 Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn Ser Thr
227 65 70 75 80
228
229 Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala Trp Glu Asn His His
230 85 90 95
231
232 Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln
233 100 105 110
234
235 Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys
236 115 120 125
237
238 Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser
239 130 135 140
240
241 Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg
242 145 150 155 160
243
244 His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
245 165 170 175
246
247 Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro Thr
248 180 185 190
249
250 Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp
251 195 200 205
252
253 Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu Val Val Pro
254 210 215 220
255
256 Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg His Cys Trp Pro
257 225 230 235 240
258



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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text